



SEQUENCE LISTING

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de la Monte, Suzanne M.
Ince, Nedim
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#4

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<120> DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS

<130> 21486-032 DIV4

<140> 09/903,199

<141> 2001-07-11

<150> 09/436,184

<151> 1999-11-08

<160> 9

<170> PatentIn Ver. 2.1

<210> 1

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
EGF-like domain

<220>

<221> VARIANT

<222> (2)..(8)

<223> Wherein Xaa is any amino acid

<220>

<221> VARIANT

<222> (10)..(13)

<223> Wherein Xaa is any amino acid.

<220>

<221> VARIANT

<222> (15)..(24)

<223> Wherein Xaa is any amino acid.

<220>

<221> VARIANT

<222> (26)

<223> Wherein Xaa is any amino acid.

<220>

<221> VARIANT

<222> (28)..(35)

<223> Wherein Xaa is any amino acid.

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Cys
35

<210> 2

<211> 758

<212> PRT

<213> Homo sapiens

<400> 2

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Gly Ser Gly Ser Gly Ser Thr Ser Ala Gly Ser Ser Ser Pro Gly Ala
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Arg Arg Glu Thr Lys His Gly Gly His Lys Asn Gly Arg Lys Gly Gly
35 40 45

Leu Ser Gly Thr Ser Phe Phe Thr Trp Phe Met Val Ile Ala Leu Leu
50 55 60

Gly Val Trp Thr Ser Val Ala Val Val Trp Phe Asp Leu Val Asp Tyr
65 70 75 80

Glu Glu Val Leu Gly Lys Leu Gly Ile Tyr Asp Ala Asp Gly Asp Gly
85 90 95

Asp Phe Asp Val Asp Asp Ala Lys Val Leu Leu Gly Leu Lys Glu Arg
100 105 110

Ser Thr Ser Glu Pro Ala Val Pro Pro Glu Glu Ala Glu Pro His Thr
115 120 125

Glu Pro Glu Glu Gln Val Pro Val Glu Ala Glu Pro Gln Asn Ile Glu
130 135 140

Asp Glu Ala Lys Glu Gln Ile Gln Ser Leu Leu His Glu Met Val His
145 150 155 160

Ala Glu His Val Glu Gly Glu Asp Leu Gln Gln Glu Asp Gly Pro Thr
165 170 175

Gly Glu Pro Gln Gln Glu Asp Asp Glu Phe Leu Met Ala Thr Asp Val
180 185 190

Asp Asp Arg Phe Glu Thr Leu Glu Pro Glu Val Ser His Glu Glu Thr
195 200 205

Glu His Ser Tyr His Val Glu Glu Thr Val Ser Gln Asp Cys Asn Gln
210 215 220

Asp Met Glu Glu Met Met Ser Glu Gln Glu Asn Pro Asp Ser Ser Glu
225 230 235 240

Pro Val Val Glu Asp Glu Arg Leu His His Asp Thr Asp Asp Val Thr
245 250 255

Tyr Gln Val Tyr Glu Glu Gln Ala Val Tyr Glu Pro Leu Glu Asn Glu
260 265 270

Gly Ile Glu Ile Thr Glu Val Thr Ala Pro Pro Glu Asp Asn Pro Val
275 280 285

Glu Asp Ser Gln Val Ile Val Glu Glu Val Ser Ile Phe Pro Val Glu
290 295 300

Glu Gln Gln Glu Val Pro Pro Glu Thr Asn Arg Lys Thr Asp Asp Pro
305 310 315 320

Glu Gln Lys Ala Lys Val Lys Lys Lys Pro Lys Leu Leu Asn Lys
325 330 335

Phe Asp Lys Thr Ile Lys Ala Glu Leu Asp Ala Ala Glu Lys Leu Arg
340 345 350

Lys Arg Gly Lys Ile Glu Glu Ala Val Asn Ala Phe Lys Glu Leu Val
355 360 365

Arg Lys Tyr Pro Gln Ser Pro Arg Ala Arg Tyr Gly Lys Ala Gln Cys
370 375 380

Glu Asp Asp Leu Ala Glu Lys Arg Arg Ser Asn Glu Val Leu Arg Gly
385 390 395 400

Ala Ile Glu Thr Tyr Gln Glu Val Ala Ser Leu Pro Asp Val Pro Ala
405 410 415

Asp Leu Leu Lys Leu Ser Leu Lys Arg Arg Ser Asp Arg Gln Gln Phe
420 425 430

Leu Gly His Met Arg Gly Ser Leu Leu Thr Leu Gln Arg Leu Val Gln
435 440 445

Leu Phe Pro Asn Asp Thr Ser Leu Lys Asn Asp Leu Gly Val Gly Tyr
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Leu Leu Ile Gly Asp Asn Asp Asn Ala Lys Lys Val Tyr Glu Val
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Leu Ser Val Thr Pro Asn Asp Gly Phe Ala Lys Val His Tyr Gly Phe
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Ile Leu Lys Ala Gln Asn Lys Ile Ala Glu Ser Ile Pro Tyr Leu Lys
500 505 510

Glu Gly Ile Glu Ser Gly Asp Pro Gly Thr Asp Asp Gly Arg Phe Tyr
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Phe His Leu Gly Asp Ala Met Gln Arg Val Gly Asn Lys Glu Ala Tyr
530 535 540

Lys Trp Tyr Glu Leu Gly His Lys Arg Gly His Phe Ala Ser Val Trp
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Gln Arg Ser Leu Tyr Asn Val Asn Gly Leu Lys Ala Gln Pro Trp Trp
565 570 575

Thr Pro Lys Glu Thr Gly Tyr Thr Glu Leu Val Lys Ser Leu Glu Arg
580 585 590

Asn Trp Lys Leu Ile Arg Asp Glu Gly Leu Ala Val Met Asp Lys Ala
595 600 605

Lys Gly Leu Phe Leu Pro Glu Asp Glu Asn Leu Arg Glu Lys Gly Asp
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Trp Ser Gln Phe Thr Leu Trp Gln Gln Gly Arg Arg Asn Glu Asn Ala
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Cys Lys Gly Ala Pro Lys Thr Cys Thr Leu Leu Glu Lys Phe Pro Glu
645 650 655

Thr Thr Gly Cys Arg Arg Gly Gln Ile Lys Tyr Ser Ile Met His Pro
660 665 670

Gly Thr His Val Trp Pro His Thr Gly Pro Thr Asn Cys Arg Leu Arg
675 680 685

Met His Leu Gly Leu Val Ile Pro Lys Glu Gly Cys Lys Ile Arg Cys
690 695 700

Ala Asn Glu Thr Arg Thr Trp Glu Glu Gly Lys Val Leu Ile Phe Asp
705 710 715 720

Asp Ser Phe Glu His Glu Val Trp Gln Asp Ala Ser Ser Phe Arg Leu
725 730 735

Ile Phe Ile Val Asp Val Trp His Pro Glu Leu Thr Pro Gln Gln Arg
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Arg Ser Leu Pro Ala Ile
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<210> 3

<211> 2324

<212> DNA

<213> Homo sapiens

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<210> 4
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: EGF-like
cysteine-rich repeat

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<221> VARIANT
<222> (3)...(5)
<223> Wherein any Xaa may be any amino acid

<220>
<221> VARIANT
<222> (6)...(7)
<223> Wherein Xaa is any amino acid.

<220>
<221> VARIANT
<222> (10)
<223> Wherein Xaa is any amino acid.

<220>
<221> VARIANT
<222> (14)
<223> Wherein Xaa is any amino acid.

<220>
<221> VARIANT
<222> (17) .. (18)

<220>
<221> VARIANT
<222> (25) .. (26)
<223> Wherein Xaa is any amino acid.

<220>
<221> VARIANT
<222> (29)
<223> Wherein Xaa is any amino acid.

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Xaa Xaa Cys Asn Asn Ala Ala Cys Xaa Xaa Asp Gly Xaa Asp Cys
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<210> 5
<211> 1242
<212> PRT
<213> Homo sapiens

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Gly Tyr Leu Arg Lys Pro Lys Ser Met His Lys Arg Phe Phe Val Leu
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Arg Ala Ala Ser Glu Ala Gly Gly Pro Ala Arg Leu Glu Tyr Tyr Glu
35 40 45

Asn Glu Lys Lys Trp Arg His Lys Ser Ser Ala Pro Lys Arg Ser Ile
50 55 60

Pro Leu Glu Ser Cys Phe Asn Ile Asn Lys Arg Ala Asp Ser Lys Asn
65 70 75 80

Lys His Leu Val Ala Leu Tyr Thr Arg Asp Glu His Phe Ala Ile Ala
85 90 95

Ala Asp Ser Glu Ala Glu Gln Asp Ser Trp Tyr Gln Ala Leu Leu Gln
100 105 110

Leu His Asn Arg Ala Lys Gly His His Asp Gly Ala Ala Ala Leu Gly
115 120 125

Ala Gly Gly Gly Gly Ser Cys Ser Gly Ser Ser Gly Leu Gly Glu
130 135 140

Ala Gly Glu Asp Leu Ser Tyr Gly Asp Val Pro Pro Gly Pro Ala Phe
145 150 155 160

Lys Glu Val Trp Gln Val Ile Leu Lys Pro Lys Gly Leu Gly Gln Thr
165 170 175

Lys Asn Leu Ile Gly Ile Tyr Arg Leu Cys Leu Thr Ser Lys Thr Ile
180 185 190

Ser Phe Val Lys Leu Asn Ser Glu Ala Ala Ala Val Val Leu Gln Leu
195 200 205

Met Asn Ile Arg Arg Cys Gly His Ser Glu Asn Phe Phe Phe Ile Glu
210 215 220

Val Gly Arg Ser Ala Val Thr Gly Pro Gly Glu Phe Trp Met Gln Val
225 230 235 240

Asp Asp Ser Val Val Ala Gln Asn Met His Glu Thr Ile Leu Glu Ala
245 250 255

Met Arg Ala Met Ser Asp Glu Phe Arg Pro Arg Ser Lys Ser Gln Ser
260 265 270

Ser Ser Asn Cys Ser Asn Pro Ile Ser Val Pro Leu Arg Arg His His
275 280 285

Leu Asn Asn Pro Pro Pro Ser Gln Val Gly Leu Thr Arg Arg Ser Arg
290 295 300

Thr Glu Ser Ile Thr Ala Thr Ser Pro Ala Ser Met Val Gly Gly Lys
305 310 315 320

Pro Gly Ser Phe Arg Val Arg Ala Ser Ser Asp Gly Glu Gly Thr Met
325 330 335

Ser Arg Pro Ala Ser Val Asp Gly Ser Pro Val Ser Pro Thr Asn
340 345 350

Arg Thr His Ala His Arg His Arg Gly Ser Ala Arg Leu His Pro Pro
355 360 365

Leu Asn His Ser Arg Ser Ile Pro Met Pro Ala Ser Arg Cys Ser Pro
370 375 380

Ser Ala Thr Ser Pro Val Ser Leu Ser Ser Ser Thr Ser Gly His
385 390 395 400

Gly Ser Thr Ser Asp Cys Leu Phe Pro Arg Arg Ser Ser Ala Ser Val
405 410 415

Ser Gly Ser Pro Ser Asp Gly Gly Phe Ile Ser Ser Asp Glu Tyr Gly
420 425 430

Ser Ser Pro Cys Asp Phe Arg Ser Ser Phe Arg Ser Val Thr Pro Asp
435 440 445

Ser Leu Gly His Thr Pro Pro Ala Arg Gly Glu Glu Leu Ser Asn
450 455 460

Tyr Ile Cys Met Gly Gly Lys Gly Pro Ser Thr Leu Thr Ala Pro Asn
465 470 475 480

Gly His Tyr Ile Leu Ser Arg Gly Gly Asn Gly His Arg Cys Thr Pro
485 490 495

Gly Thr Gly Leu Gly Thr Ser Pro Ala Leu Ala Gly Asp Glu Ala Ala
500 505 510

Ser Ala Ala Asp Leu Asp Asn Arg Phe Arg Lys Arg Thr His Ser Ala
515 520 525

Gly Thr Ser Pro Thr Ile Thr His Gln Lys Thr Pro Ser Gln Ser Ser
530 535 540

Val Ala Ser Ile Glu Glu Tyr Thr Glu Met Met Pro Ala Tyr Pro Pro
545 550 555 560

Gly Gly Gly Ser Gly Gly Arg Leu Pro Gly His Arg His Ser Ala Phe
565 570 575

Val Pro Thr Arg Ser Tyr Pro Glu Glu Gly Leu Glu Met His Pro Leu
580 585 590

Glu Arg Arg Gly Gly His His Arg Pro Asp Ser Ser Thr Leu His Thr
595 600 605

Asp Asp Gly Tyr Met Pro Met Ser Pro Gly Val Ala Pro Val Pro Ser
610 615 620

Gly Arg Lys Gly Ser Gly Asp Tyr Met Pro Met Ser Pro Lys Ser Val
625 630 635 640

Ser Ala Pro Gln Gln Ile Ile Asn Pro Ile Arg Arg His Pro Gln Arg
645 650 655

Val Asp Pro Asn Gly Tyr Met Met Ser Pro Ser Gly Gly Cys Ser
660 665 670

Pro Asp Ile Gly Gly Pro Ser Ser Ser Ser Ser Asn Ala
675 680 685

Val Pro Ser Gly Thr Ser Tyr Gly Lys Leu Trp Thr Asn Gly Val Gly
690 695 700

Gly His His Ser His Val Leu Pro His Pro Lys Pro Pro Val Glu Ser
705 710 715 720

Ser Gly Gly Lys Leu Leu Pro Cys Thr Gly Asp Tyr Met Asn Met Ser
725 730 735

Pro Val Gly Asp Ser Asn Thr Ser Ser Pro Ser Asp Cys Tyr Tyr Gly
740 745 750

Pro Glu Asp Pro Gln His Lys Pro Val Leu Ser Tyr Tyr Ser Leu Pro
755 760 765

Arg Ser Phe Lys His Thr Gln Arg Pro Gly Glu Pro Glu Glu Gly Ala
770 775 780

Arg His Gln His Leu Arg Leu Ser Thr Ser Ser Gly Arg Leu Leu Tyr
785 790 795 800

Ala Ala Thr Ala Asp Asp Ser Ser Ser Ser Thr Ser Ser Asp Ser Leu
805 810 815

Gly Gly Gly Tyr Cys Gly Ala Arg Leu Glu Pro Ser Leu Pro His Pro
820 825 830

His His Gln Val Leu Gln Pro His Leu Pro Arg Lys Val Asp Thr Ala
835 840 845

Ala Gln Thr Asn Ser Arg Leu Ala Arg Pro Thr Arg Leu Ser Leu Gly
850 855 860

Asp Pro Lys Ala Ser Thr Leu Pro Arg Ala Arg Glu Gln Gln Gln
865 870 875 880

Gln Gln Pro Leu Leu His Pro Pro Glu Pro Lys Ser Pro Gly Glu Tyr
885 890 895

Val Asn Ile Glu Phe Gly Ser Asp Gln Ser Gly Tyr Leu Ser Gly Pro
900 905 910

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915 920 925

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930 935 940

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945 950 955 960

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1060 1065 1070

Thr Arg Val Asn Leu Ser Pro Asn Arg Asn Gln Ser Ala Lys Val Ile
1075 1080 1085

Arg Ala Asp Pro Gln Gly Cys Arg Arg Arg His Ser Ser Glu Thr Phe
1090 1095 1100

Ser Ser Thr Pro Ser Ala Thr Arg Val Gly Asn Thr Val Pro Phe Gly
1105 1110 1115 1120

Ala Gly Ala Ala Val Gly Gly Gly Ser Ser Ser Ser Glu
1125 1130 1135

Asp Val Lys Arg His Ser Ser Ala Ser Phe Glu Asn Val Trp Leu Arg
1140 1145 1150

Pro Gly Glu Leu Gly Gly Ala Pro Lys Glu Pro Ala Lys Leu Cys Gly
1155 1160 1165

Ala Ala Gly Gly Leu Glu Asn Gly Leu Asn Tyr Ile Asp Leu Asp Leu
1170 1175 1180

Val Lys Asp Phe Lys Gln Cys Pro Gln Glu Cys Thr Pro Glu Pro Gln
1185 1190 1195 1200

Pro Pro Pro Pro Pro Pro His Gln Pro Leu Gly Ser Gly Glu Ser
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Ser Ser Thr Arg Arg Ser Ser Glu Asp Leu Ser Ala Tyr Ala Ser Ile
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Ser Phe Gln Lys Gln Pro Glu Asp Arg Gln
1235 1240

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<211> 5828
<212> DNA
<213> Homo sapiens

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16